

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/509,954  
Source: PCT/0  
Date Processed by STIC: 1/9/06

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PCT

**RAW SEQUENCE LISTING**  
**PATENT APPLICATION: US/10/509,954**

**DATE: 01/09/2006**  
**TIME: 11:22:12**

**Input Set : A:\32436ASEQLIST.TXT**  
**Output Set: N:\CRF4\01092006\J509954.raw**

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4 <110> APPLICANT: Barclay, Jane
5      Buxton, Francis Paul
6      Ganju, Pamposh
7      Natt, Francois Jean-Charles
8      Song, Chuanzheng
9
10     Weiler, Jan
11     Wishart, William Leonard
12 <120> TITLE OF INVENTION: Use of MOB-5 in Pain
13 <130> FILE REFERENCE: PN/4-32436A
14 <140> CURRENT APPLICATION NUMBER: 10/509,954
15 <141> CURRENT FILING DATE: 2004-10-04
16 <150> PRIOR APPLICATION NUMBER: PCT/EP03/03469
17 <151> PRIOR FILING DATE: 2003-04-02
18 <150> PRIOR APPLICATION NUMBER: 60/369,893
19 <151> PRIOR FILING DATE: 2002-04-03
20 <160> NUMBER OF SEQ ID NOS: 20
21 <170> SOFTWARE: FastSEQ for Windows Version 4.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 29
24 <212> TYPE: DNA
25 <213> ORGANISM: Artificial Sequence
26 <220> FEATURE:
27 <223> OTHER INFORMATION: Primer Sequences for Rat MOB-5 gene
28 <400> SEQUENCE: 1
29 atgcagacaa gcttgagaca acagattct
30 <210> SEQ ID NO: 2
31 <211> LENGTH: 27
32 <212> TYPE: DNA
33 <213> ORGANISM: Artificial Sequence
34 <220> FEATURE:
35 <223> OTHER INFORMATION: Primer Sequences for Rat MOB-5 gene
36 <400> SEQUENCE: 1
37 tcagagctgg tagaaattct gcatcca
38 <210> SEQ ID NO: 3
39 <211> LENGTH: 393
40 <212> TYPE: DNA
41 <213> ORGANISM: Rattus
42 <220> FEATURE:
43 <221> NAME/KEY: prim_transcript
44 <222> LOCATION: (28)...(48)
45 <223> OTHER INFORMATION: Gene Specific Primer Sequence designed from Rat
46     MOB-5 gene
47 <221> NAME/KEY: prim_transcript
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64 <222> LOCATION: (175) ... (198)  
 65 <223> OTHER INFORMATION: Gene Specific Primer Sequence designed from Rat  
 66 MOB-5 gene  
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 70 catatccctg ttgtcctcag ggcacttcag acccttgccc atggaccctt gtcgttggct 120  
 71 caggctttc ttcagacaccc accttttagt ccaaacgaca gccatggaca gcacctttgg 180  
 72 atgctccgac tgaccacaa cgtggatttg catatttattt acagccctat ttaactaatg 240  
 73 tcactgttc ggttagaaaacc ggtattttt tgtgagactg gacgttccat gaaagcatca 300  
 74 tgccccgtgt ttgcaccta cttcctgtga gctggctcac catggggca gtagatggtt 360  
 75 gctcagtaaa tatttaaat ggaaaaaaaaaaa aaa 393  
 77 <210> SEQ ID NO: 4  
 78 <211> LENGTH: 21  
 79 <212> TYPE: DNA  
 80 <213> ORGANISM: Artificial Sequence  
 82 <220> FEATURE:  
 83 <223> OTHER INFORMATION: RT-PCR Primer region for rat MOB-5 gene  
 85 <400> SEQUENCE: 4  
 86 cctttgttct ccgtggcatt t 21  
 88 <210> SEQ ID NO: 5  
 89 <211> LENGTH: 23  
 90 <212> TYPE: DNA  
 91 <213> ORGANISM: Artificial Sequence  
 93 <220> FEATURE:  
 94 <223> OTHER INFORMATION: RT-PCR Primer region for rat MOB-5 geneMOB-5 gene  
 96 <400> SEQUENCE: 5  
 97 ctttggatgc tccgactgac cca 23  
 99 <210> SEQ ID NO: 6  
 100 <211> LENGTH: 183  
 101 <212> TYPE: PRT  
 102 <213> ORGANISM: Rattus  
 104 <220> FEATURE:  
 105 <221> NAME/KEY: PEPTIDE  
 106 <222> LOCATION: (1) ... (183)  
 107 <223> OTHER INFORMATION: Amino Acid sequence corresponding to the Open  
 108 Reading Frame region deduced from MOB-5 cDNAs  
 109 Cloned from Rattus Dorsal Root Ganglia  
 111 <400> SEQUENCE: 6  
 112 Met Gln Thr Ser Leu Arg Gln Gln Ile Leu Pro Gly Leu Ser Leu Ile  
 113 1 5 10 15  
 114 Leu Leu Val Leu Ser Gln Val Pro Glu Leu Gln Gly Gln Glu Phe Arg  
 115 20 25 30  
 116 Phe Gly Pro Cys Gln Val Thr Gly Val Val Leu Pro Glu Leu Trp Glu  
 117 35 40 45  
 118 Ala Phe Trp Thr Val Lys Asn Thr Val Lys Thr Gln Asp Glu Leu Thr  
 119 50 55 60  
 120 Ser Val Arg Leu Leu Lys Pro Gln Val Leu Gln Asn Val Ser Asp Ala  
 121 65 70 75 80  
 122 Glu Ser Cys Tyr Leu Ala His Ser Leu Leu Lys Phe Tyr Leu Asn Thr

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123	85	90	95
124	Val Phe Lys Asn Tyr His Ser Glu Ile Val Lys Phe Lys Val Leu Lys		
125	100	105	110
126	Ser Phe Ser Thr Leu Ala Asn Asn Phe Leu Val Ile Met Ser Lys Leu		
127	115	120	125
128	Gln Pro Ser Lys Asp Asn Ala Met Leu Pro Ile Ser Asp Ser Ala Arg		
129	130	135	140
130	Arg Arg Phe Leu Leu Phe His Arg Thr Phe Lys Gln Leu Asp Ile Glu		
131	145	150	155
132	160	165	170
133	Val Ala Leu Ala Lys Ala Phe Gly Glu Val Asp Ile Leu Leu Ala Trp		
134	175		
135	Met Gln Asn Phe Tyr Gln Leu		
136	180		
138	<210> SEQ ID NO: 7		
139	<211> LENGTH: 18		
140	<212> TYPE: DNA		
141	<213> ORGANISM: Artificial Sequence		
143	<220> FEATURE:		
144	<223> OTHER INFORMATION: Antisense Oligonucleotide		
W-->	146 <221> NAME/KEY: modified_base		
147	<222> LOCATION: 1-5, 14-18		
148	<223> OTHER INFORMATION: modified with 2'-O-(2-methoxyethyl)		
W-->	150 <221> modified_base		
151	<222> LOCATION: 6-13		
152	<223> OTHER INFORMATION: modified with a phosphorothioate group		
W-->	154 <221> modified_base		
155	<222> LOCATION: 2,5,16		
156	<223> OTHER INFORMATION: m5c		
W-->	158 <400> 7		
159	tcagcaggct gtgggcaa	18	
161	<210> SEQ ID NO: 8		
162	<211> LENGTH: 18		
163	<212> TYPE: DNA		
164	<213> ORGANISM: Artificial Sequence		
166	<220> FEATURE:		
167	<223> OTHER INFORMATION: Antisense Oligonucleotide		
W-->	169 <221> NAME/KEY: modified_base		
170	<222> LOCATION: 1-5, 14-18		
171	<223> OTHER INFORMATION: modified with 2'-O-(2-methoxyethyl) group		
W-->	173 <221> modified_base		
174	<222> LOCATION: 6-13		
175	<223> OTHER INFORMATION: modified with phosphorothioate group		
W-->	177 <221> modified_base		
178	<222> LOCATION: 2-3, 16		
179	<223> OTHER INFORMATION: m5c		
W-->	181 <400> 8		
182	tccgaaggcg gtgtgcaa	18	
184	<210> SEQ ID NO: 9		
185	<211> LENGTH: 18		

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186 <212> TYPE: DNA
187 <213> ORGANISM: Artificial Sequence
189 <220> FEATURE:
190 <223> OTHER INFORMATION: Antisense oligonucleotide
W--> 192 <221> NAME/KEY: modified_base
193 <222> LOCATION: 1-5, 14-18
194 <223> OTHER INFORMATION: modified with 2'-O-(2-methoxyethyl) group
W--> 196 <221> modified_base
197 <222> LOCATION: 2,5, 16
198 <223> OTHER INFORMATION: m5c
W--> 200 <400> 9
201 tcagcaggct gtggcaa
203 <210> SEQ ID NO: 10
204 <211> LENGTH: 18
205 <212> TYPE: DNA
206 <213> ORGANISM: Artificial Sequence
208 <220> FEATURE:
209 <223> OTHER INFORMATION: Antisense oligonucleotide
W--> 211 <221> NAME/KEY: modified_base
212 <222> LOCATION: 1-5, 14-18
213 <223> OTHER INFORMATION: modified with 2'-O-(2-methoxyethyl) group
W--> 215 <221> modified_base
216 <222> LOCATION: 2,3, 16
217 <223> OTHER INFORMATION: m5c
W--> 219 <400> 10
220 tccgaaggcg gtgtcaa
222 <210> SEQ ID NO: 11
223 <211> LENGTH: 549
224 <212> TYPE: DNA
225 <213> ORGANISM: Rattus
227 <220> FEATURE:
228 <221> NAME/KEY: gene
229 <222> LOCATION: (1)...(549)
230 <223> OTHER INFORMATION: Rat MOB-5 cDNA
232 <400> SEQUENCE: 11
233 atgcagacaa gctttagaca acagattctc cccggcctga gcctaattct ttcgttttg 60
234 agccaagtac cagagttca gggtaagag ttccgatttgc ggccttgcga agtgaccggg 120
235 gtggttctcc cagaactgtg ggaggccttc tggactgtga agaacactgt gaaaactcag 180
236 gacgagctca caagtgtccg gctgttggaa ccacaggttc tgcagaatgt ctggatgcc 240
237 gagagctgtt accttgcaca cagcctgtg aagttctact tgaacactgt tttcaaaaaac 300
238 tatcacagcg aaatagtcaa attcaagggtc ttgaagtcat ttcacttgc gccaacaac 360
239 ttttagtca tcatgtccaa actgcagcct agtaaggaca atgccatgtc tccattttgt 420
240 gacagtgcac gccggcggtt tttgtgttc cacagaacat tcaaacagtt ggacatagaa 480
241 gtggctttgg cgaaagcctt tggggaaagtg gacattctcc tggcctggat gcagaatttc 540
242 taccagctc
244 <210> SEQ ID NO: 12
245 <211> LENGTH: 21
246 <212> TYPE: DNA
247 <213> ORGANISM: Artificial Sequence

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RAW SEQUENCE LISTING DATE: 01/09/2006  
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Input Set : A:\32436ASEQLIST.TXT  
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249 <220> FEATURE:
250 <223> OTHER INFORMATION: Antisense Oligoribonucleotides sequence to rat
251 MOB-5 gene
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254 <222> LOCATION: 1-18
255 <223> OTHER INFORMATION: phosphodiester internucleotide linkage
W--> 257 <221> modified_base
258 <222> LOCATION: 19-21
259 <223> OTHER INFORMATION: deoxyribonucleoside internucleotide linkage
W--> 261 <400> 12
262 uucagcaggc uguggggcaag g 21
264 <210> SEQ ID NO: 13
265 <211> LENGTH: 21
266 <212> TYPE: DNA
267 <213> ORGANISM: Artificial Sequence
269 <220> FEATURE:
270 <223> OTHER INFORMATION: Sense Oligoribonucleotides sequence to rat MOB-5
271 gene
W--> 273 <221> NAME/KEY: modified_base
274 <222> LOCATION: 1-18
275 <223> OTHER INFORMATION: phosphodiester internucleotide linlkage
W--> 277 <221> modified_base
278 <222> LOCATION: 19-21
279 <223> OTHER INFORMATION: deoxyribobnucleoside internucleotide linkagechm5u
W--> 281 <400> 13
282 uugcccacag ccugcugaat t 21
284 <210> SEQ ID NO: 14
285 <211> LENGTH: 21
286 <212> TYPE: DNA
287 <213> ORGANISM: Artificial Sequence
289 <220> FEATURE:
290 <223> OTHER INFORMATION: Mismatch Antisense Oligoribonucleotides to rat
291 MOB-5 gene
W--> 293 <221> NAME/KEY: modified_base
294 <222> LOCATION: 1-18
295 <223> OTHER INFORMATION: phosphodiester internucleotide linkages
W--> 297 <221> modified_base
298 <222> LOCATION: 19-21
299 <223> OTHER INFORMATION: deoxyribose internucleotide linages
W--> 301 <400> 14
302 uuccgaaggc ggugugcaag g 21
304 <210> SEQ ID NO: 15
305 <211> LENGTH: 21
306 <212> TYPE: DNA
307 <213> ORGANISM: Artificial Sequence
309 <220> FEATURE:
310 <223> OTHER INFORMATION: Mismatch Sense oligoribonucleotides to rat MOB-5
311 gene
W--> 313 <221> NAME/KEY: modified_base

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VERIFICATION SUMMARY  
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Input Set : A:\32436ASEQLIST.TXT  
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L:146 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:150 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7  
L:154 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7  
L:158 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7  
L:169 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:173 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:8  
L:177 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:8  
L:181 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:8  
L:192 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:196 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:9  
L:200 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:9  
L:211 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:215 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10  
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L:253 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:257 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12  
L:261 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12  
L:273 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:277 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:13  
L:281 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:13  
L:293 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:297 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:14  
L:301 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:14  
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L:337 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:16  
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L:357 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:17  
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L:373 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:377 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:18  
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L:393 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:397 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:19  
L:401 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:19  
L:413 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:417 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:20  
L:421 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:20